RAW SEQUENCE LISTING PATENT APPLICATION US/09/055, 145A

DATE: 10/26/98 TIME: 11:25:12

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This Raw Listing contains the General Information Section and up to the first pages.

ENTERED SEQUENCE LISTING 1 2 General Information: 3 (1) 5 (i) APPLICANT: Weeks, Donald P. 6 Wang, Xiao-Zhuo Herman, Patricia L. 7 8 9 (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS" 10 11 (iii) NUMBER OF SEQUENCES: 6 12 RECEIVED 13 14 (iv) CORRESPONDENCE ADDRESS: 15 (A) ADDRESSEE: Sheridan Ross P.C. 16 (B) STREET: 1700 Lincoln St., Suite 3500 17 (C) CITY: Denver TECHCENTER 1600/2900 (D) STATE: Colorado 18 19 (E) COUNTRY: USA 20 (F) ZIP: 80203 21 (V) COMPUTER READABLE FORM: 22 23 (A) MEDIUM TYPE: Floppy disk 24 (B) COMPUTER: IBM PC compatible 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 27 (vi) CURRENT APPLICATION DATA: 28 (A) APPLICATION NUMBER: 29 30 (B) FILING DATE: 31 (C) CLASSIFICATION: 32 33 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/042,666 34 35 (B) FILING DATE: 04-APR-1997 36 37 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/042,941 38 39 (B) FILING DATE: 04-APR-1997 40 41 (viii) ATTORNEY/AGENT INFORMATION: 42 (A) NAME: Crook, Wannell M. 43 (B) REGISTRATION NUMBER: 31,071 44 (C) REFERENCE/DOCKET NUMBER: 3553-18 45 46 (ix) TELECOMMUNICATION INFORMATION:

RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

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47 48		(A) TELEPHONE: (303) 863-9700 (B) TELEFAX: (303) 863-0223
49		(b) Indiana. (505) 005 0225
50		
51	(2) INFORM	MATION FOR SEQ ID NO:1:
52	,	~
53	(i) S	SEQUENCE CHARACTERISTICS:
54		(A) LENGTH: 29 amino acids
55		(B) TYPE: amino acid
56		(C) STRANDEDNESS: single
57		(D) TOPOLOGY: linear
58		
59	(ii) N	OLECULE TYPE: protein
60		
61		
62	(ix) E	FEATURE:
63		(A) NAME/KEY: Region
64		(B) LOCATION: 28
65	ml #	(D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or
66	Thr"	
67 68	/ie/ I	ים איינוסי.
69	(IX) I	PEATURE: (A) NAME/KEY: Region
70		(B) LOCATION: 29
71		(D) OTHER INFORMATION: /note= "Best quess for Xaa = Pro"
72		(b) officer the officer of the control of the contr
73		
74	(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:1:
75	, ,	
76	Thr H	Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu Leu
77	1	5 10 15
78		
79	Ser (Slu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa
80		20 25
81		
82	(2) INFORM	MATION FOR SEQ ID NO:2:
83		NECURNAL GUARAGERTAMIAG.
84	(1)	SEQUENCE CHARACTERISTICS:
85 86		(A) LENGTH: 20 amino acids
86 87		(B) TYPE: amino acid (C) STRANDEDNESS: single
88		(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear
89		(b) Torologi: Timear
90	/ i i \ N	MOLECULE TYPE: protein
91	(11)	obboom iii protein
92		
93	(ix) H	PEATURE:
94	(/	(A) NAME/KEY: Region
95		(B) LOCATION: 8
96		(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
97		•
98	(ix) H	FEATURE:
99		(A) NAME/KEY: Region

RAW SEQUENCE LISTING PATENT APPLICATION US/09/055, 145A

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105			•	,		ION:												
106			(D) OI	THER	INF	DRMAT	CION	: /n	ote=	"Bes	st gi	ıess	for	Xaa	= Cy	's"	
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108		(ix)	FEA	TURE	፤:													
109			(A) N.	AME/I	KEY:	Regi	on										
110			(B	i LO	CAT	ION:	20											
111			•					TON	: /n	ote=	"Bes	st ai	iess	for	Xaa	= Cy	'S"	
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113																		
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114		(XI)	SEQ	OENC	E DE	SOCK.	IPTIC	JN: 2	SEQ.	ID M	J: Z:							
115						1 ~1	_			- 1	_		_	_				
116			Tyr	val	L va.		r Asp) Ala	а хаа	a 116		s Xaa	а г.у.	s Ty:	r Me	t Asp	хаа	
117		1				5					10					15		
118																		
119		Val	Glu	Va]	L Xaa	Э												
120					20													
121															\rightarrow	_		
122	(2)	INFO	RMAT	ION	FOR	SEQ	ID N	10:3:	:							1.6.	W.	
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124		(i)	SEQ	UENC	CE CE	HARA	CTERI	STIC	cs:								1 C.	
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126 127) TY													•	
127			(C) S7	RANI	DEDNI	ESS:	sing								i	•	
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127 128 129		/;;\	(C) ST	rani Polo	DEDNI DGY:	ESS: line	sing ear								i rou _{ger}	· W	
127 128 129 130		(ii)	(C) ST	rani Polo	DEDNI DGY:	ESS:	sing ear								i mayor	· W	
127 128 129 130 131		(ii)	(C) ST	rani Polo	DEDNI DGY:	ESS: line	sing ear									W:	
127 128 129 130 131		. ,	(C)) ST	TRANI DPOLO	DEDNI DGY:	ESS: line	sing ear								i waye	v;	
127 128 129 130 131 132 133		(ii) (ix)	(C) (D) MOL	ECUI	TRANI DPOLO LE TY	DEDNI DGY: YPE:	ESS: line cDNA	sing ear								i mu _{ga}	et;	
127 128 129 130 131 132 133 134		. ,	(C) (D) MOL	ECUI	TRANI DPOLO LE TY E:	DEDNI DGY: YPE: KEY:	ESS: line CDNA	sing ear								i way n	w;	
127 128 129 130 131 132 133		. ,	(C) (D) MOL	ECUI	TRANI DPOLO LE TY E:	DEDNI DGY: YPE: KEY:	ESS: line cDNA	sing ear								i waye	w;	
127 128 129 130 131 132 133 134		. ,	(C) (D) MOL	ECUI	TRANI DPOLO LE TY E:	DEDNI DGY: YPE: KEY:	ESS: line CDNA	sing ear								v_{xy}	w	
127 128 129 130 131 132 133 134 135		. ,	(C) (D) MOL	ECUI	TRANI DPOLO LE TY E:	DEDNI DGY: YPE: KEY:	ESS: line CDNA	sing ear								i way e	u;	
127 128 129 130 131 132 133 134 135		(ix)	(C (D MOL FEA (A	ECUI	TRANI DPOLO LE TY E: AME/I DCAT	DEDNI DGY: YPE: KEY: ION:	ESS: line CDNA	sing ear	gle	ID NO	D:3:					i ray e	w	
127 128 129 130 131 132 133 134 135 136		(ix)	(C (D MOL FEA (A	ECUI	TRANI DPOLO LE TY E: AME/I DCAT	DEDNI DGY: YPE: KEY: ION:	ESS: line cDNA CDS	sing ear	gle	ID NO	D:3:					i euge	u;	
127 128 129 130 131 132 133 134 135 136 137	ATG	(ix)	MOL FEA (A (B	ECUI	FRANI DPOLO LE TY E: AME/I DCATI	DEDNI DGY: YPE: KEY: ION:	ESS: line cDNA CDS l1	sinq ear .020	gle			GCG					u;	48
127 128 129 130 131 132 133 134 135 136 137 138		(ix) (xi)	(C) (D) MOL FEA (A) (B) SEQ	ECUI TURE) NA) LO	FRANICE TY E: AME/I CCAT CGC	DEDNI DGY: YPE: KEY: ION: ESCR:	ESS: line cDNA CDS ll	singear .020 DN: S	gle EEQ TAT	GTG	GCG		CTG	ccc	GAG	GAA	W	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141	Met	(ix)	(C) (D) MOL FEA (A) (B) SEQ	ECUI TURE) NA) LO	TRANIDPOLO LE TY E: AME/I DCATI CE DI CGC Arg	DEDNI DGY: YPE: KEY: ION: ESCR:	ESS: line cDNA CDS ll	singear .020 DN: S	gle EEQ TAT	GTG Val	GCG		CTG	ccc	G A G Glu	GAA	w	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142		(ix) (xi)	(C) (D) MOL FEA (A) (B) SEQ	ECUI TURE) NA) LO	FRANICE TY E: AME/I CCAT CGC	DEDNI DGY: YPE: KEY: ION: ESCR:	ESS: line cDNA CDS ll	singear .020 DN: S	gle EEQ TAT	GTG	GCG		CTG	ccc	GAG	GAA	w	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143	Met 1	(ix) (xi) ACC Thr	MOL FEA (A (B SEQ TTC	TURE TURE TURE OUENCE GTC Val	TRANIDPOLO LE TY E: AME/I DCATT CE DI CGC Arg 5	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASN	ESS: line cDNA CDS ll IPTIC GCC Ala	sing ear .020 DN: S TGG Trp	SEQ : TAT Tyr	GTG Val 10	GCG Ala	Ala	CTG Leu	CCC Pro	GAG Glu 15	GAA Glu	w	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	Met 1 CTG	(ix) (xi) ACC Thr	MOL FEA (A (B SEQ TTC Phe	TURE TURE OUENCE GTC Val	TRANIDPOLO LE TY LE: AME/I DCATT CGC Arg 5	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASn	ESS: line cDNA CDS ll IPTIC GCC Ala	singear .020 TGG Trp	SEQ : TAT Tyr	GTG Val 10	GCG Ala	Ala	CTG Leu ACA	CCC Pro	GAG Glu 15 CTC	GAA Glu GCG	w	4 8
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	Met 1 CTG	(ix) (xi) ACC Thr	MOL FEA (A (B SEQ TTC Phe	TURE OUENCE AAG Lys	TRANIDPOLO LE TY LE: AME/I DCATT CGC Arg 5	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASn	ESS: line cDNA CDS ll IPTIC GCC Ala	singear .020 TGG Trp	SEQ TAT Tyr ACG Thr	GTG Val 10	GCG Ala	Ala	CTG Leu ACA	CCC Pro	GAG Glu 15 CTC	GAA Glu GCG	w	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	Met 1 CTG	(ix) (xi) ACC Thr	MOL FEA (A (B SEQ TTC Phe	TURE TURE OUENCE GTC Val	TRANIDPOLO LE TY LE: AME/I DCATT CGC Arg 5	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASn	ESS: line cDNA CDS ll IPTIC GCC Ala	singear .020 TGG Trp	SEQ : TAT Tyr	GTG Val 10	GCG Ala	Ala	CTG Leu ACA	CCC Pro	GAG Glu 15 CTC	GAA Glu GCG	· · · · · · · · · · · · · · · · · · ·	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	Met 1 CTG Leu	(ix) (xi) ACC : Thr :	MOL FEA (A (B SEQ TTC Phe	TURE TURE () NA () LO () CUENC GTC Val AAG Lys 20	E: AME/I DCATE CGC Arg 5 CCG Pro	DEDNI DGY: YPE: XEY: ION: ESCR: AAT Asn CTC Leu	CDS CDNA CDS 11 CPTIC GCC Ala	Since ar A C C C C C C C C C C C C C C C C C C	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	· · · · · · · · · · · · · · · · · · ·	96
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	Met 1 CTG Leu	(ix) (xi) ACC : Thr : TCC : Ser :	MOL FEA (A (B SEQ TTC Phe GAA Glu	TURE () NA () NA () LO () CUENC () CAG	E: AME/I CCAT CCG Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT Asn CTC Leu	CDS CDNA CDS 11 CPTIC GCC Ala GGC Gly	singear .020 TGG Trp CGG Arg	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30 GAC	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	· · · · · · · · · · · · · · · · · · ·	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149	Met 1 CTG Leu	(ix) (xi) ACC : Thr :	MOL FEA (A (B SEQ TTC Phe GAA Glu CGC Arg	TURE () NA () NA () LO () CUENC () CAG	E: AME/I CCAT CCG Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT Asn CTC Leu	CDS CDNA CDS 11 CPTIC GCC Ala GGC Gly	Since ar A A A A A A A A A A A A A A A A A A	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30 GAC	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	ur.	96
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150	Met 1 CTG Leu	(ix) (xi) ACC : Thr : TCC : Ser :	MOL FEA (A (B SEQ TTC Phe GAA Glu	TURE () NA () NA () LO () CUENC () CAG	E: AME/I CCAT CCG Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT Asn CTC Leu	CDS CDNA CDS 11 CPTIC GCC Ala GGC Gly	singear .020 TGG Trp CGG Arg	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30 GAC	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	· · · · · · · · · · · · · · · · · · ·	96
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151	Met 1 CTG Leu CTC Leu	(ix) (xi) ACC : Thr : TCC : Ser : TAC : Tyr :	MOL FEA (A (B SEQ TTC Phe GAA Glu CGC Arg 35	TURE () NA () LO () LO () CAG (GIn	CCC Pro	DEDNI DGY: YPE: XEY: ION: ESCR: AAT ASN CTC Leu	CDS CDNA CDS 11 IPTIC GCC Ala GGC Gly	Since ar A A A A A A A A A A A A A A A A A A	SEQ TAT Tyr ACG Thr 25 GTC Val	GTG Val 10 ATT Ile GCG Ala	GCG Ala CTC Leu GCG Ala	Ala GAC Asp CTG Leu	CTG Leu ACA Thr CTC Leu 45	CCC Pro CCG Pro 30 GAC Asp	GAG Glu 15 CTC Leu ATC	GAA Glu GCG Ala TGT Cys	· · · · · · · · · · · · · · · · · · ·	96 144
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150	Met 1 CTG Leu CTC Leu	(ix) (xi) ACC : Thr : TCC : Ser :	MOL FEA (A (B SEQ TTC Phe GAA Glu CGC Arg 35	TURE () NA () LO () LO () CAG (GIn	CCC Pro	DEDNI DGY: YPE: XEY: ION: ESCR: AAT ASN CTC Leu	CDS CDNA CDS 11 IPTIC GCC Ala GGC Gly	Since ar A A A A A A A A A A A A A A A A A A	SEQ TAT Tyr ACG Thr 25 GTC Val	GTG Val 10 ATT Ile GCG Ala	GCG Ala CTC Leu GCG Ala	Ala GAC Asp CTG Leu	CTG Leu ACA Thr CTC Leu 45	CCC Pro CCG Pro 30 GAC Asp	GAG Glu 15 CTC Leu ATC	GAA Glu GCG Ala TGT Cys	· · · · · · · · · · · · · · · · · · ·	96

RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

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160 161 162 163						GGC Gly									288
164 165 166 167						GTG Val									336
168 169 170 171						GCC Ala									384
172 173 174 175						TAT Tyr									432
176 177 178 179						CTG Leu 150									480
180 181 182 183						GCC Ala									528
184 185 186 187						GTC Val									576
188 189 190 191						CCG Pro									624
192 193 194 195						GAC Asp									672
196 197 198 199						TTC Phe 230									720
200 201 202 203						TCG Ser									768
204						TAT Tyr									816

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206
208 GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG 209 Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala 210 275 280 285 211 212 CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC 213 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg 214 290 295 300 215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
209 Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala 210 275 280 285 211 212 CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC 213 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg 214 290 295 300 215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
210 275 280 285 211 212 CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC 912 213 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg 214 290 295 300 215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
212 CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC 213 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg 214 290 295 300 215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
Leu Val Lys Glu Asp Lys Val Val Glu Ala Ile Glu Arg Arg Arg 214 290 295 300 215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
214 290 295 300 215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 960 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
215 216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TGC GAC 960 217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
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210 303 310 313
219
220 GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC 1008
221 Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
222 325 330 335
223
224 GAA GCC GCC TGA 1020
225 Glu Ala Ala *
226 340
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229 (2) INFORMATION FOR SEQ ID NO:4: 230
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 339 amino acids
233 (B) TYPE: amino acid
234 (D) TOPOLOGY: linear
235
236 (ii) MOLECULE TYPE: protein
237
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
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240 Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu 241 1 5 10 15
242
243 Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
244 20 25 30
245
246 Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
247 35 40 45
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249 Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
250 50 55 60 251
251 252 Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
252 Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys 253 65 70 75 80
253 65 /0 /3 60
255 Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
256 85 90 95
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258 Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro

SEQUENCE VERIFICATION REPORT PATENT APPLICATION *US/09/055,145A*

DATE: 10/26/98 TIME: 11:25:17

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